

SEQUENCE LISTING

<110> Conklin, Darrell C.
 Blumberg, Hal
 Deisher, Theresa A.

<120> A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219C

<130> 97-64C1

<150> US 60/066,157

<151> 1997-11-19

<150> US 09/186,342

<151> 1998-11-04

<160> 19

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)...(889)

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gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca gggacctacg	120
gcacctgctg gaccacctg cttctccat cgaagcaggg aagtgggagc ctcgagccct	180
cgggtggaag ctgaccccaa gccacccttc acctggacag g atg aga gtg tca ggt	236
Met Arg Val Ser Gly	
1 5	

gtg ctt cgc ctc ctg gcc ctc atc ttt gcc ata gtc acg aca tgg atg	284
Val Leu Arg Leu Leu Ala Leu Ile Phe Ala Ile Val Thr Thr Trp Met	
10 15 20	

ttt att cga agc tac atg agc ttc agc atg aaa acc atc cgt ctg cca	332
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Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	Met	Lys	Thr	Ile	Arg	Leu	Pro	
			25					30					35			
cgc	tgg	ctg	gcc	tcg	ccc	acc	aag	gag	atc	cag	gtt	aaa	aag	tac	aag	380
Arg	Trp	Leu	Ala	Ser	Pro	Thr	Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	
		40					45					50				
tgt	ggc	ctc	atc	aag	ccc	tgc	cca	gcc	aac	tac	ttt	gcg	ttt	aaa	atc	428
Cys	Gly	Leu	Ile	Lys	Pro	Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	
	55					60				65						
tgc	agt	ggg	gcc	gcc	aac	gtc	gtg	ggc	cct	act	atg	tgc	ttt	gaa	gac	476
Cys	Ser	Gly	Ala	Ala	Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	
70					75				80						85	
cgc	atg	atc	atg	agt	cct	gtg	aaa	aac	aat	gtg	ggc	aga	ggc	cta	aac	524
Arg	Met	Ile	Met	Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	
				90				95						100		
atc	gcc	ctg	gtg	aat	gga	acc	acg	gga	gct	gtg	ctg	gga	cag	aag	gca	572
Ile	Ala	Leu	Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	
			105					110					115			
ttt	gac	atg	tac	tct	gga	gat	gtt	atg	cac	cta	gtg	aaa	ttc	ctt	aaa	620
Phe	Asp	Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	
	120						125					130				
gaa	att	ccg	ggg	ggc	gca	ctg	gtg	ctg	gtg	gcc	tcc	tac	gac	gat	cca	668
Glu	Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	
	135					140				145						
ggg	acc	aaa	atg	aac	gat	gaa	agc	agg	aaa	ctc	ttc	tct	gac	ttg	ggg	716
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	Gly	
150					155					160					165	
agt	tcc	tac	gca	aaa	caa	ctg	ggc	ttc	cgg	gac	agc	tgg	gtc	ttc	ata	764
Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	Phe	Ile	
				170				175						180		
gga	gcc	aaa	gac	ctc	agg	ggc	aaa	agc	ccc	ttt	gag	cag	ttc	tta	aag	812
Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	Phe	Leu	Lys	
			185				190						195			

aac agc cca gac aca aac aaa tac gag gga tgg cca gag ctg ctg gag 860
 Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro Glu Leu Leu Glu
 200 205 210

atg gag ggc tgc atg ccc ccg aag cca tt ttaggggtggc tgtggctctt 909
 Met Glu Gly Cys Met Pro Pro Lys Pro
 215 220

cctcagccag gggcctgaag aagctcctgc ctgacttagg agtcagagcc cggcaggggc 969
 tgaggaggag gagcaggggg tgctgcgtgg aagggtgctgc aggtccttgc acgctgtgtc 1029
 gcgcctctcc tcctcggaac cagaaccctc ccacagcaca tcctaccgag aagaccagcc 1089
 tcagaggggtc cttctggaac cagctgtctg tggagagaat ggggtgcttt cgtcagggac 1149
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<211> 223

<212> PRT

<213> Homo sapiens

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Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala Ile
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 20 25 30
 Thr Ile Arg Leu Pro Arg Trp Leu Ala Ser Pro Thr Lys Glu Ile Gln
 35 40 45
 Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro Cys Pro Ala Asn Tyr
 50 55 60
 Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala Asn Val Val Gly Pro Thr
 65 70 75 80
 Met Cys Phe Glu Asp Arg Met Ile Met Ser Pro Val Lys Asn Asn Val
 85 90 95
 Gly Arg Gly Leu Asn Ile Ala Leu Val Asn Gly Thr Thr Gly Ala Val
 100 105 110
 Leu Gly Gln Lys Ala Phe Asp Met Tyr Ser Gly Asp Val Met His Leu
 115 120 125
 Val Lys Phe Leu Lys Glu Ile Pro Gly Gly Ala Leu Val Leu Val Ala
 130 135 140
 Ser Tyr Asp Asp Pro Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu
 145 150 155 160
 Phe Ser Asp Leu Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp
 165 170 175

Ser Trp Val Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe
 180 185 190
 Glu Gln Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp
 195 200 205
 Pro Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 210 215 220

<210> 3
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Z219c polypeptide Motif 1

<400> 3
 Phe Asp Met
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<210> 4
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Z219c polypeptide Motif 2

<400> 4
 Tyr Asp Asp
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<210> 5
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Z219c polypeptide Motif 3

<400> 5
 Leu Gly Ser
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<210> 6
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Z219c polypeptide Motif 4

<400> 6
 Trp Val Phe
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<210> 7
 <211> 3
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<220>
 <223> Z219c polypeptide Motif 5

<400> 7
 Glu Gly Cys
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<210> 8
 <211> 669
 <212> DNA
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<220>
 <223> Degenerate polynucleotide sequence of z219c

<221> variation
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 <223> N is any nucleotide

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 atgmgngrnw sngngnnytn nmgnnytnytn gcnytnatht tygcnathgt nacnacntgg 60
 atgttyathm gnwsntayat gwsnttywsn atgaaracna thmgnytncc nmgnrtggytn 120
 gcnwsnccna cnaargarat hcargtnaar aartayaart gyggnytnat haarccntgy 180
 ccngcnaayt aytygcntt yaarathtgy wsngngngcng cnaaygtngt nggnccnacd 240
 atgtgyttyg argaymgnat gathatgwsn ccngtnaara ayaaygtngg nmgnngnytn 300
 aayathgcny tngtnaaygg nacnacnggn gcngtnytn gncaraargc nttygayatg 360

taywsnggng aygtnatgca yytngtnaar ttyytnaarg arathccngg nggngcnytn	420
gtnytngtng cnwsntayga ygayccnggn acnaaratga aygaygarws nmгнаarytn	480
ttywsngayy tnggnwsnws ntaygcnaar carytnggnt tymnggayws ntgggtntty	540
athggngcna argayytnmg nggnaarwsn ccnttygarc arttyytnaa raaywsnccn	600
gayacnaaya artaygargg ntggccngar ytnytngara tggarggntg yatgccnccn	660
aarcntty	669

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<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC694

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taatacgact cactataggg	20
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<212> DNA

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<223> Oligonucleotide primer ZC695

<400> 10

gatttaggtg acactatag	19
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<210> 11

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC13978

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ggcggcccca ctgcagattt taaac	25
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<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC15288

<400> 12

ttggctgggc agggcttgat gag

23

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC14067

<400> 13

tggccatccc tcgtatttgt t

21

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC14068

<400> 14

ccctgcccag ccaactactt t

21

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC14869

<400> 15

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21

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC14868

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21

<210> 17

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<212> PRT

<213> Mus musculus

<400> 17

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Pro	Gln	Leu	Leu	Leu	Asn	Phe	Leu	Thr	Glu	Ile	Pro	Asp	Ser	Thr	Leu
			20					25					30		
Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	Gly	Thr	Lys	Met	Asn	Asp	Lys
		35					40					45			
Ile	Lys	Thr	Leu	Phe	Ser	Asn	Leu	Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu
	50					55					60				
Gly	Phe	Arg	Asp	Ser	Trp	Val	Phe	Val	Gly	Ala	Lys	Asp	Leu	Lys	Ser
65					70				75					80	
Lys	Ser	Pro	Tyr	Glu	Gln	Phe	Leu	Lys	Asn	Asn	Pro	Glu	Thr	Asn	Lys
				85					90					95	
Tyr	Asp	Gly	Trp	Pro	Glu	Leu	Leu	Glu	Leu	Glu	Gly	Cys	Val	Pro	Arg
			100					105					110		
Lys	Val	Met													
		115													

<210> 18

<211> 230

<212> PRT

<213> Homo sapiens

<400> 18

Met	Arg	Leu	Ala	Gly	Pro	Leu	Arg	Ile	Val	Val	Leu	Val	Val	Ser	Val
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			20					25					30		

<210> 19
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<212> PRT
<213> Homo sapiens

<400> 19

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Leu Leu Thr Phe Tyr Val Ile Ser Gln Val Phe Glu Ile Lys Met Asp
20 25 30
Ala Ser Leu Gly Asn Leu Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala
35 40 45
Arg Ser Thr Lys Pro Pro Arg Tyr Lys Cys Gly Ile Ser Lys Ala Cys
50 55 60

<213> Homo sapiens

<400> 19

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Leu	Leu	Thr	Phe	Tyr	Val	Ile	Ser	Gln	Val	Phe	Glu	Ile	Lys	Met	Asp
			20					25					30		
Ala	Ser	Leu	Gly	Asn	Leu	Phe	Ala	Arg	Ser	Ala	Leu	Asp	Thr	Ala	Ala
		35					40					45			
Arg	Ser	Thr	Lys	Pro	Pro	Arg	Tyr	Lys	Cys	Gly	Ile	Ser	Lys	Ala	Cys
	50					55					60				

Pro Glu Lys His Phe Ala Phe Lys Met Ala Ser Gly Ala Ala Asn Val
 65 70 75 80
 Val Gly Pro Lys Ile Cys Leu Glu Asp Asn Val Leu Met Ser Gly Val
 85 90 95
 Lys Asn Asn Val Gly Arg Gly Ile Asn Val Ala Leu Ala Asn Gly Lys
 100 105 110
 Thr Gly Glu Val Leu Asp Thr Lys Tyr Phe Asp Met Trp Gly Gly Asp
 115 120 125
 Val Ala Pro Phe Ile Glu Phe Leu Lys Ala Ile Gln Asp Gly Thr Ile
 130 135 140
 Val Leu Met Gly Thr Tyr Asp Asp Gly Ala Thr Lys Leu Asn Asp Glu
 145 150 155 160
 Ala Arg Arg Leu Ile Ala Asp Leu Gly Ser Thr Ser Ile Thr Asn Leu
 165 170 175
 Gly Phe Arg Asp Asn Trp Val Phe Cys Gly Gly Lys Gly Ile Lys Thr
 180 185 190
 Lys Ser Pro Phe Glu Gln His Ile Lys Asn Asn Lys Asp Thr Asn Lys
 195 200 205
 Tyr Glu Gly Trp Pro Glu Val Val Glu Met Glu Gly Cys Ile Pro Gln
 210 215 220
 Lys Gln Asp
 225